



SEQUENCE LISTING

<110> Zeneca Limited

<120> Insecticidal Proteins from Paecilomyces and Synergistic  
Combinations Thereof

<130> SYN-128

<140> US 10/019,823

<141> 2001-12-21

<150> PCT/GB00/02457

<151> 2000-06-23

<150> GB 9915215.9

<151> 1999-06-29

<150> GB 9930536.9

<151> 1999-12-23

<160> 65

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 33

<212> PRT

<213> Paecilomyces sp.

<220>

<221> VARIANT

<222> 1, 2

<223> Xaa = Any Amino Acid

<400> 1

Xaa Xaa Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala Leu Pro  
1 5 10 15  
Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys Val Cys  
20 25 30  
Arg

<210> 2

<211> 33

<212> PRT

<213> Paecilomyces sp.

<400> 2

Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala Leu Pro  
1 5 10 15  
Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys Val Cys  
20 25 30  
Arg

<210> 3

<211> 35

<212> PRT  
<213> Paecilomyces sp.

<220>  
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<222> 1, 2  
<223> Xaa = Any Amino Acid

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Xaa Xaa Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala  
1 5 10 15  
Leu Pro Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys  
20 25 30  
Val Cys Arg  
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<210> 4  
<211> 332  
<212> DNA  
<213> Paecilomyces sp.

<400> 4  
ggcaagatct gcaactcctgc tggagttgta cgtatttttca tccattttcct ycaccactcc 60  
tctaacatga agcaactttc tcttctctct agaaatgtcc cgcggctctt ccttgctgcc 120  
ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tggatctggc aagcgagacc 180  
ataacatgac gcagtatact aaccctggcc gttatagaac aaggttgtga gtogacatgt 240  
tktacaacct ctacaaacgc gcgcactaat gacaacggta gtgccggtaa ttctagtgtc 300  
gcaacttttg agcgtgggat aagtatgctt cg 332

<210> 5  
<211> 320  
<212> DNA  
<213> Paecilomyces sp.

<400> 5  
gggaaaattt gtacgccggc ggggggttgta cgtatttctca tccattttcct ccaccactcc 60  
tctaacatga agcaactctc tcttctctct agaaatgtcc cgcggctctt ccttgctgcc 120  
ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tctgacacg acgtgaaggc 180  
aatgtactga ccctggccgt tatagaacaa ggttgtgagt cgacatgttt tacaacctct 240  
acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgtcgc aacttttgag 300  
cgtgggataa gtatgcttcg 320

<210> 6  
<211> 320  
<212> DNA  
<213> Paecilomyces sp.

<400> 6  
gggaaaattt gtacgccggc ggggggttgta cgtatttttca tccattttcct ccaccactcc 60  
tctaacatga agcaactctc tcttctctct araaatgtcc cgcggctctt ccttgctgcc 120  
ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tctgacacg acgtgaaggc 180  
aatgtactga ccctggccgt tatagaacaa ggttgtgagt cgacatgttt tacaacctct 240  
acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgtcgc aacttttgag 300  
cgtgggataa gtatgcttcg 320

<210> 7  
<211> 174  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide codon optimised

<400> 7

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atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggcaagat ctgcaccccg gccggcgtga agtgcccggc cgccctcccg 120
tgctgcccgg gcctccgctg catcgcgggc gtgaacaaca aggtgtgccg ctga 174
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<210> 8

<211> 174

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide codon optimised

<400> 8

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gagatccagg ccggtaaaat ttgtaccccg gccggcgtga agtgcccggc cgccctcccg 120
tggtgtccgg gcctcagggtg tattggtggt gtgaataata aagtgtgtcg ctga 174
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<210> 9

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence containing intron sequence

<400> 9

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atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggcaagat ctgcactcct gctggagttg tttgtttctg cttctacctt 120
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaattttata acttttctaa tatatgacca aaacatggtg atgttttagaa atgtcccgcg 300
gctcttcctt gctgccccgg acttcgctgc atcggcggcg tcaacaacaa ggtttgccgg 360
taa 363
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<210> 10

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 10

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gagatccagg cctcctacgg caagatctgc actcctgctg gagttgtttg tttctgcttc 120
tacctttgat atatatataa taattatcat taattagtag taatataata tttcaaatat 180
ttttttcaaa ataaaagaat gtagtatata gcaattgctt ttctgtagtt tataagtgtg 240
tatattttta tttataactt ttctaataa tgacaaaaac atggtgatgt ttagaaatgt 300
cccgcggctc ttctttgctg ccccggaact cgctgcatcg gcggcgtcaa caacaaggtt 360
tgccggtaa 369
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<210> 11

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 11

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gagatccagg cctcctacat ctgcactcct gctggagttg tttgtttctg cttctacctt 120
tgatataatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatgggt atgttttagaa atgtcccgcg 300
gctcttccct gctgccccgg acttcgctgc atcggcgggc tcaacaacaa ggtttgccgg 360
taa 363
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<210> 12

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence containing intron and codon  
optimised

<400> 12

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atgggtggca gcggcagggc tgctctgctg ctggcccttg tggccgtgag cctggccgtg 60
gagatccagg cgggcaagat ctgcaccccg gccggcgtgg tttgtttctg cttctacctt 120
tgatataatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatgggt atgttttagaa gtgccccggc 300
gccctcccggt gctgccccgg cctccgctgc atcggcgggc tgaacaacaa ggtgtgccgc 360
tga 363
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<210> 13

<211> 439

<212> DNA

<213> *Paecilomyces* sp.

<400> 13

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aaatctccgc cgtcattgtc gcactcttgc ccagcgccgc catggccggc aagatctgca 120
ctcctgctgg agttgtacgt attttcatcc atttccctca ccactcctct aacatgaagc 180
aactttctct tctctctaga aatgtccgcg ggtcttctct tgtgccccg gacttcgctg 240
catcggcggc gtcaacgtaa gtcaccatgg atctggcaag cgagaccata acatgacgca 300
gtatactaac cctggccggt atagaacaag gttgtgagtc gacatgttkt acaacctcta 360
caaacgcgcg cactaatgac aacggtagtg ccggtaattc tagtgtcgca acttttgagc 420
gtgggataag tatgcttcg 439
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<210> 14

<211> 102

<212> DNA

<213> *Paecilomyces* sp.

<400> 14

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cttcgctgca tcggcgccgt caacaacaag gtttgccggt aa 102
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<210> 15

<211> 84

<212> DNA

<213> *Dahlia* sp.

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 tcagatattg cttctgtttc agga 84

<210> 16  
 <211> 87  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Radish signal sequence

<400> 16  
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 ttggaagctc caactatggg tgaagct 87

<210> 17  
 <211> 72  
 <212> DNA  
 <213> Zea mays

<400> 17  
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 gagatccagg cc 72

<210> 18  
 <211> 90  
 <212> DNA  
 <213> Nicotiana sp.

<400> 18  
 atgggatttg ttctcttttc acaattgcct tcatttcttc ttgtctctac acttctctta 60  
 ttcttagtaa tatccactc ttgccgtgcc 90

<210> 19  
 <211> 51  
 <212> DNA  
 <213> Paecilomyces sp.

<400> 19  
 atgcaaactc ccgccgtcat tgctgcactc ttgccagcg ccgccatggc c 51

<210> 20  
 <211> 28  
 <212> PRT  
 <213> Dahlia sp.

<400> 20  
 Met Val Asn Arg Ser Val Ala Phe Ser Ala Phe Val Leu Ile Leu Phe  
 1 5 10 15  
 Val Leu Ala Ile Ser Asp Ile Ala Ser Val Ser Gly  
 20 25

<210> 21  
 <211> 29  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Radish protein target sequence

<400> 21

Met Ala Lys Phe Ala Ser Ile Ile Ala Leu Leu Phe Ala Ala Leu Val  
1 5 10 15  
Leu Phe Ala Ala Phe Glu Ala Pro Thr Met Val Glu Ala  
20 25

<210> 22

<211> 24

<212> PRT

<213> Zea Mays

<400> 22

Met Gly Gly Ser Gly Arg Ala Ala Leu Leu Leu Ala Leu Val Ala Val  
1 5 10 15  
Ser Leu Ala Val Glu Ile Gln Ala  
20

<210> 23

<211> 30

<212> PRT

<213> Nicotiana sp.

<400> 23

Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser  
1 5 10 15  
Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala  
20 25 30

<210> 24

<211> 17

<212> PRT

<213> Paecilomyces sp.

<400> 24

Met Gln Ile Ser Ala Val Ile Val Ala Leu Phe Ala Ser Ala Ala Met  
1 5 10 15  
Ala

<210> 25

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 25

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44

<210> 26

<211> 19

<212> DNA

<213> Artificial Sequence

<220>  
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 <400> 26  
 .tcgggctcgc atgaattcg 19  
  
 <210> 27  
 <211> 18  
 <212> DNA  
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 <400> 27  
 atgaattcgc ggccgcat 18  
  
 <210> 28  
 <211> 21  
 <212> DNA  
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 <223> Primers  
  
 <400> 28  
 tcgggctcgc atgaattcgc g 21  
  
 <210> 29  
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 ctcgcatgaa ttcgcggccg c 21  
  
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 <221> misc\_feature  
 <222> 9, 12, 15  
 <223> n = A,T,C or G  
  
 <400> 30  
 athtgyacnc cngcngg 17  
  
 <210> 31  
 <211> 20  
 <212> DNA  
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 <221> misc\_feature  
 <222> 9, 12, 15, 18  
 <223> n = A,T,C or G  
  
 <400> 31  
 athtgyacnc cngcnggngt 20  
  
 <210> 32  
 <211> 17  
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 <223> Primers  
  
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 <222> 3, 6, 9, 12, 15  
 <223> n = A,T,C or G  
  
 <400> 32  
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 <210> 33  
 <211> 17  
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 <223> Primers  
  
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 <222> 3, 12, 15  
 <223> n = A,T,C or G  
  
 <400> 33  
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 <210> 34  
 <211> 16  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Primers  
  
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 <222> 2, 14  
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 <210> 35  
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 <212> DNA  
 <213> Artificial Sequence



<220>  
 <223> Primers  
  
 <221> misc\_feature  
 <222> 3, 6, 18  
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 <210> 36  
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 <212> DNA  
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 <221> misc\_feature  
 <222> 12, 15, 18, 21, 24  
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 <210> 37  
 <211> 26  
 <212> DNA  
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 <222> 3, 6, 9, 12, 21, 24  
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 ccngcnggng tnaartgycc ngcngc 26  
  
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 <222> 23, 24, 25, 26, 27  
 <223> n = A,T,C or G  
 <400> 43  
 ggtttaatta cccaagtttg agnnnnn 27  
 <210> 44  
 <211> 22

<212> DNA  
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 <210> 45  
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 <210> 46  
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 <212> DNA  
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 <400> 46  
 taattacca agtttgag 18  
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 ggtttaatta cccaagtttg ag 22  
 <210> 48  
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 <222> 3, 15, 18, 21  
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<210> 50

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<210> 54

<211> 718

<212> PRT

<213> Artificial Sequence

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<223> PROTEIN cry1Ia1 Embl. Accession No. X62821

<221> VARIANT  
 <222> 602  
 <223> Xaa = Any Amino Acid

<400> 54

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			20					25					30		
Glu	Leu	Gln	Asn	Ile	Asn	His	Glu	Asp	Cys	Leu	Lys	Met	Ser	Glu	Tyr
		35					40					45			
Glu	Asn	Val	Glu	Pro	Phe	Val	Ser	Ala	Ser	Thr	Ile	Gln	Thr	Gly	Ile
	50					55					60				
Gly	Ile	Ala	Gly	Lys	Ile	Leu	Gly	Thr	Leu	Gly	Val	Pro	Phe	Ala	Gly
65					70					75					80
Gln	Val	Ala	Ser	Leu	Tyr	Ser	Phe	Ile	Leu	Gly	Glu	Leu	Trp	Pro	Lys
				85					90					95	
Gly	Lys	Asn	Gln	Trp	Glu	Ile	Phe	Met	Glu	His	Val	Glu	Glu	Ile	Ile
			100					105					110		
Asn	Gln	Lys	Ile	Ser	Thr	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Thr	Asp	Leu
		115					120					125			
Lys	Gly	Leu	Gly	Asp	Ala	Leu	Ala	Val	Tyr	His	Asp	Ser	Leu	Glu	Ser
	130					135					140				
Trp	Val	Gly	Asn	Arg	Asn	Asn	Thr	Arg	Ala	Arg	Ser	Val	Val	Lys	Ser
145					150					155					160
Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe
				165					170					175	
Ala	Val	Ser	Gly	Glu	Glu	Val	Pro	Leu	Leu	Pro	Ile	Tyr	Ala	Gln	Ala
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Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Ile	Phe	Gly	Lys
	195						200					205			
Glu	Trp	Gly	Leu	Ser	Ser	Ser	Glu	Ile	Ser	Thr	Phe	Tyr	Asn	Arg	Gln
	210					215					220				
Val	Glu	Arg	Ala	Gly	Asp	Tyr	Ser	Tyr	His	Cys	Val	Lys	Trp	Tyr	Ser
225					230					235					240
Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Glu	Ser	Trp	Val	Arg
				245					250					255	
Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val
			260					265					270		
Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Gln	Met	Tyr	Pro	Ile	Lys	Thr	Thr
		275					280					285			
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His
	290					295				300					
Pro	His	Pro	Ser	Phe	Thr	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro
305					310					315					320
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Val	Arg	Asn	Pro	His	Leu	Leu
				325					330					335	
Asp	Phe	Leu	Glu	Gln	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser
		340						345					350		
Asn	Thr	Gln	Tyr	Met	Asn	Met	Trp	Gly	Gly	His	Lys	Leu	Glu	Phe	Arg
		355					360					365			
Thr	Ile	Gly	Gly	Thr	Leu	Asn	Ile	Ser	Thr	Gln	Gly	Ser	Thr	Asn	Thr
	370					375					380				
Ser	Ile	Asn	Pro	Val	Thr	Leu	Pro	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg
385					390					395					400
Thr	Glu	Ser	Leu	Ala	Gly	Leu	Asn	Leu	Phe	Leu	Thr	Gln	Pro	Val	Asn
				405					410					415	
Val	Pro	Arg	Val	Asp	Phe	His	Trp	Lys	Phe	Val	Thr	His	Pro	Ile	Ala
			420					425					430		
Ser	Asp	Asn	Phe	Tyr	Tyr	Pro	Gly	Tyr	Ala	Gly	Ile	Gly	Thr	Gln	Leu

	435		440		445										
Gln	Asp	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Glu	Ala	Thr	Gly	Gln	Pro	Asn
	450				455						460				
Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ser	Ala
465					470					475					480
Ser	His	Val	Lys	Ala	Leu	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala	Asp
			485						490					495	
Arg	Thr	Asn	Thr	Ile	Glu	Pro	Asn	Ser	Ile	Thr	Gln	Ile	Pro	Leu	Val
			500					505					510		
Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro	Gly
	515						520					525			
Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe	Gly
	530					535					540				
Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg	Val
545					550					555					560
Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser	Ile
			565					570						575	
Asn	Gly	Lys	Ala	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn	Arg
			580					585					590		
Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Xaa	Thr	Val	Gly	Phe	Thr	Thr
	595					600						605			
Pro	Phe	Ser	Leu	Leu	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala	Trp
	610					615					620				
Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val
625					630					635					640
Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala	Gln
			645						650					655	
Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu	Lys
		660					665						670		
Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu
	675						680						685		
Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe	Glu
	690					695					700				
Ile	Val	Lys	Tyr	Ala	Lys	Gln	Leu	His	Ile	Glu	Arg	Asn	Met		
705					710					715					

<210> 55

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ia2 Embl. Accession No. M98544

<400> 55

Met	Lys	Leu	Lys	Asn	Gln	Asp	Lys	His	Gln	Ser	Phe	Ser	Ser	Asn	Ala
1				5					10					15	
Lys	Val	Asp	Lys	Ile	Ser	Thr	Asp	Ser	Leu	Lys	Asn	Glu	Thr	Asp	Ile
			20				25						30		
Glu	Leu	Gln	Asn	Ile	Asn	His	Glu	Asp	Cys	Leu	Lys	Met	Ser	Glu	Tyr
		35				40					45				
Glu	Asn	Val	Glu	Pro	Phe	Val	Ser	Ala	Ser	Thr	Ile	Gln	Thr	Gly	Ile
	50					55					60				
Gly	Ile	Ala	Gly	Lys	Ile	Leu	Gly	Thr	Leu	Gly	Val	Pro	Phe	Ala	Gly
65				70					75					80	
Gln	Val	Ala	Ser	Leu	Tyr	Ser	Phe	Ile	Leu	Gly	Glu	Leu	Trp	Pro	Lys
			85					90					95		
Gly	Lys	Asn	Gln	Trp	Glu	Ile	Phe	Met	Glu	His	Val	Glu	Glu	Ile	Ile
			100				105						110		

Asn	Gln	Lys	Ile	Ser	Thr	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Thr	Asp	Leu	
		115					120					125				
Lys	Gly	Leu	Gly	Asp	Ala	Leu	Ala	Val	Tyr	His	Asp	Ser	Leu	Glu	Ser	
	130					135					140					
Trp	Val	Gly	Asn	Arg	Asn	Asn	Thr	Arg	Ala	Arg	Ser	Val	Val	Lys	Ser	
	145				150					155					160	
Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe	
			165						170					175		
Ala	Val	Ser	Gly	Glu	Glu	Val	Pro	Leu	Leu	Pro	Ile	Tyr	Ala	Gln	Ala	
		180						185					190			
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Ile	Phe	Gly	Lys	
	195					200						205				
Glu	Trp	Gly	Leu	Ser	Ser	Ser	Glu	Ile	Ser	Thr	Phe	Tyr	Asn	Arg	Gln	
	210					215					220					
Val	Glu	Arg	Ala	Gly	Asp	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Ser	
	225				230					235					240	
Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Glu	Ser	Trp	Val	Arg	
			245						250					255		
Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val	
		260						265					270			
Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Gln	Met	Tyr	Pro	Ile	Lys	Thr	Thr	
	275						280					285				
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His	
	290					295					300					
Pro	His	Pro	Ser	Phe	Thr	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro	
	305				310					315					320	
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Val	Arg	Asn	Pro	His	Leu	Leu	
			325					330						335		
Asp	Phe	Leu	Glu	Gln	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser	
		340						345					350			
Asn	Thr	Gln	Tyr	Met	Asn	Met	Trp	Gly	Gly	His	Lys	Leu	Glu	Phe	Arg	
	355					360						365				
Thr	Ile	Gly	Gly	Thr	Leu	Asn	Ile	Ser	Thr	Gln	Gly	Ser	Thr	Asn	Thr	
	370					375					380					
Ser	Ile	Asn	Pro	Val	Thr	Leu	Pro	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg	
	385				390					395					400	
Thr	Glu	Ser	Leu	Ala	Gly	Leu	Asn	Leu	Phe	Leu	Thr	Gln	Pro	Val	Asn	
			405						410					415		
Gly	Val	Pro	Arg	Val	Asp	Phe	His	Trp	Lys	Phe	Val	Thr	His	Pro	Ile	
		420						425					430			
Ala	Ser	Asp	Asn	Phe	Tyr	Tyr	Pro	Gly	Tyr	Ala	Gly	Ile	Gly	Thr	Gln	
	435						440					445				
Leu	Gln	Asp	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Glu	Ala	Thr	Gly	Gln	Pro	
	450					455					460					
Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ser	
	465				470					475					480	
Ala	Ser	His	Val	Lys	Ala	Leu	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala	
			485						490					495		
Asp	Arg	Thr	Asn	Thr	Ile	Glu	Pro	Asn	Ser	Ile	Thr	Gln	Ile	Pro	Leu	
		500						505					510			
Val	Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro	
	515						520					525				
Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe	
	530				535						540					
Gly	Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg	
	545				550					555					560	
Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser	
			565						570					575		
Ile	Asn	Gly	Lys	Ala	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn	
		580						585						590		

Arg	Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Arg	Thr	Val	Gly	Phe	Thr
	595						600					605			
Thr	Pro	Phe	Ser	Phe	Leu	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala
	610					615					620				
Trp	Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe
	625				630					635					640
Val	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala
			645						650					655	
Gln	Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu
			660					665					670		
Lys	Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val
		675					680					685			
Glu	Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe
	690					695					700				
Glu	Ile	Val	Lys	Tyr	Ala	Lys	Gln	Leu	His	Ile	Glu	Arg	Asn	Met	
	705				710					715					

<210> 56

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ia3 Embl. Accession No. L36338

<400> 56

Met	Lys	Leu	Lys	Asn	Gln	Asp	Lys	His	Gln	Ser	Phe	Ser	Ser	Asn	Ala
1				5					10					15	
Lys	Val	Asp	Lys	Ile	Ser	Thr	Asp	Ser	Leu	Lys	Asn	Glu	Thr	Asp	Ile
			20					25					30		
Glu	Leu	Gln	Asn	Ile	Asn	His	Glu	Asp	Cys	Leu	Lys	Met	Ser	Glu	Tyr
		35					40					45			
Glu	Asn	Val	Glu	Pro	Phe	Val	Ser	Ala	Ser	Thr	Ile	Gln	Thr	Gly	Ile
	50					55					60				
Gly	Ile	Ala	Gly	Lys	Ile	Leu	Gly	Thr	Leu	Gly	Val	Pro	Phe	Ala	Gly
	65				70				75						80
Gln	Val	Ala	Ser	Leu	Tyr	Ser	Phe	Ile	Leu	Gly	Glu	Leu	Trp	Pro	Lys
			85						90					95	
Gly	Lys	Asn	Gln	Trp	Glu	Ile	Phe	Met	Glu	His	Val	Glu	Glu	Ile	Ile
			100					105						110	
Asn	Gln	Lys	Ile	Ser	Thr	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Thr	Asp	Leu
		115					120					125			
Lys	Gly	Leu	Gly	Asp	Ala	Leu	Ala	Val	Tyr	His	Asp	Ser	Leu	Glu	Ser
	130					135					140				
Trp	Val	Gly	Asn	Arg	Asn	Asn	Thr	Arg	Ala	Arg	Ser	Val	Val	Lys	Ser
	145				150					155					160
Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe
			165						170					175	
Ala	Val	Ser	Gly	Glu	Glu	Val	Pro	Leu	Leu	Pro	Ile	Tyr	Ala	Gln	Ala
			180					185					190		
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Ile	Phe	Gly	Lys
		195					200					205			
Glu	Trp	Gly	Leu	Ser	Ser	Ser	Glu	Ile	Ser	Thr	Phe	Tyr	Asn	Arg	Gln
	210					215					220				
Val	Glu	Arg	Ala	Gly	Asp	Tyr	Ser	Tyr	His	Cys	Val	Lys	Trp	Tyr	Ser
	225				230					235					240
Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Glu	Ser	Trp	Val	Arg
			245						250					255	
Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val





<211> 719  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> PROTEIN cryIIa4 Embl. Accession No. L49391

<400> 57

Met	Lys	Leu	Lys	Asn	Gln	Asp	Lys	His	Gln	Ser	Phe	Ser	Ser	Asn	Ala	1	5	10	15
Lys	Val	Asp	Lys	Ile	Ser	Thr	Asp	Ser	Leu	Lys	Asn	Glu	Thr	Asp	Ile	20	25	30	
Glu	Leu	Gln	Asn	Ile	Asn	His	Glu	Asp	Cys	Leu	Lys	Met	Ser	Glu	Tyr	35	40	45	
Glu	Asn	Val	Glu	Pro	Phe	Val	Ser	Ala	Ser	Thr	Ile	Gln	Thr	Gly	Ile	50	55	60	
Gly	Ile	Ala	Gly	Lys	Ile	Leu	Gly	Thr	Leu	Gly	Val	Pro	Phe	Ala	Gly	65	70	75	80
Gln	Val	Ala	Ser	Leu	Tyr	Ser	Phe	Ile	Leu	Gly	Glu	Leu	Trp	Pro	Lys	85	90	95	
Gly	Lys	Asn	Gln	Trp	Glu	Ile	Phe	Met	Glu	His	Val	Glu	Glu	Ile	Ile	100	105	110	
Asn	Gln	Lys	Ile	Ser	Thr	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Thr	Asp	Leu	115	120	125	
Lys	Gly	Leu	Gly	Asp	Ala	Leu	Ala	Val	Tyr	His	Asp	Ser	Leu	Glu	Ser	130	135	140	
Trp	Val	Gly	Asn	Arg	Asn	Asn	Thr	Arg	Ala	Arg	Ser	Val	Val	Lys	Ser	145	150	155	160
Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe	165	170	175	
Ala	Val	Ser	Gly	Glu	Glu	Val	Pro	Leu	Leu	Pro	Ile	Tyr	Ala	Gln	Ala	180	185	190	
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Ile	Phe	Gly	Lys	195	200	205	
Glu	Trp	Gly	Leu	Ser	Ser	Ser	Glu	Ile	Ser	Thr	Phe	Tyr	Asn	Arg	Gln	210	215	220	
Val	Glu	Arg	Ala	Gly	Asp	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Ser	225	230	235	240
Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Glu	Ser	Trp	Val	Arg	245	250	255	
Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val	260	265	270	
Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Gln	Met	Tyr	Pro	Ile	Lys	Thr	Thr	275	280	285	
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His	290	295	300	
Pro	His	Pro	Ser	Phe	Thr	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro	305	310	315	320
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Val	Arg	Asn	Pro	His	Leu	Leu	325	330	335	
Asp	Phe	Leu	Glu	Gln	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser	340	345	350	
Asn	Thr	Gln	Tyr	Met	Asn	Met	Trp	Gly	Gly	His	Lys	Leu	Glu	Phe	Arg	355	360	365	
Thr	Ile	Gly	Gly	Thr	Leu	Asn	Ile	Ser	Thr	Gln	Gly	Ser	Thr	Asn	Thr	370	375	380	
Ser	Ile	Asn	Pro	Val	Thr	Leu	Pro	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg	385	390	395	400
Thr	Glu	Ser	Leu	Ala	Gly	Leu	Asn	Leu	Phe	Leu	Thr	Gln	Pro	Val	Asn	405	410	415	

Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile  
                   420                  425                  430  
 Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Val Gly Ile Gly Thr Gln  
                   435                  440                  445  
 Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro  
                   450                  455                  460  
 Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser  
                   465                  470                  475                  480  
 Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala  
                   485                  490                  495  
 Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu  
                   500                  505                  510  
 Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro  
                   515                  520                  525  
 Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe  
                   530                  535                  540  
 Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg  
                   545                  550                  555                  560  
 Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser  
                   565                  570                  575  
 Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn  
                   580                  585                  590  
 Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr  
                   595                  600                  605  
 Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala  
                   610                  615                  620  
 Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe  
                   625                  630                  635                  640  
 Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala  
                   645                  650                  655  
 Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu  
                   660                  665                  670  
 Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val  
                   675                  680                  685  
 Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe  
                   690                  695                  700  
 Glu Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met  
                   705                  710                  715

<210> 58

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ia5 Embl. Accession No. Y08920

<400> 58

Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala  
   1                  5                  10                  15  
 Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile  
                   20                  25                  30  
 Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr  
                   35                  40                  45  
 Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile  
                   50                  55                  60  
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly  
                   65                  70                  75                  80  
 Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys





Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Lys	Ser	Trp	Val	Arg	
			245						250					255		
Tyr	Asn	Gln	Phe	Arg	Lys	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val	
			260					265					270			
Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Leu	Val	Tyr	Pro	Ile	Lys	Thr	Thr	
		275					280					285				
Ser	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His	
	290					295					300					
Pro	Asn	Gln	Ala	Phe	Ala	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro	
305					310					315					320	
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Ile	Arg	Ser	Pro	His	Leu	Leu	
			325						330					335		
Asp	Phe	Leu	Glu	Lys	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser	
		340						345					350			
Asn	Thr	Gln	Tyr	Met	Asn	Met	Trp	Gly	Gly	His	Arg	Leu	Glu	Ser	Arg	
		355					360					365				
Pro	Ile	Gly	Gly	Ala	Leu	Asn	Thr	Ser	Thr	Gln	Gly	Ser	Thr	Asn	Thr	
	370					375					380					
Ser	Ile	Asn	Pro	Val	Thr	Leu	Gln	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg	
385					390					395					400	
Thr	Glu	Ser	Leu	Ala	Gly	Leu	Asn	Leu	Phe	Leu	Thr	Gln	Pro	Val	Asn	
			405						410					415		
Gly	Val	Pro	Arg	Val	Asp	Phe	His	Trp	Lys	Phe	Pro	Thr	Leu	Pro	Ile	
			420					425					430			
Ala	Ser	Asp	Asn	Phe	Tyr	Tyr	Leu	Gly	Tyr	Ala	Gly	Val	Gly	Thr	Gln	
		435					440				445					
Leu	Gln	Asp	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Glu	Thr	Thr	Gly	Gln	Pro	
	450					455					460					
Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ser	
465					470					475					480	
Ala	Ser	His	Val	Lys	Ala	Leu	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala	
			485						490					495		
Asp	Arg	Thr	Asn	Thr	Ile	Glu	Pro	Asn	Ser	Ile	Thr	Gln	Ile	Pro	Leu	
			500					505					510			
Val	Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro	
		515					520					525				
Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe	
	530					535					540					
Gly	Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg	
545					550					555					560	
Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser	
			565						570					575		
Ile	Asn	Gly	Lys	Ala	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn	
		580						585					590			
Arg	Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Arg	Thr	Ile	Gly	Phe	Thr	
		595					600					605				
Thr	Pro	Phe	Ser	Phe	Ser	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala	
	610					615					620					
Trp	Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	
625					630					635					640	
Val	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala	
			645						650					655		
Gln	Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu	
		660						665					670			
Lys	Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	
		675					680					685				
Glu	Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe	
	690					695					700					
Glu	Ile	Val	Lys	Tyr	Ala	Lys	Gln	Ile	His	Ile	Glu	Arg	Asn	Met		
705					710					715						

<210> 60  
 <211> 33  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PROTEIN

<221> VARIANT  
 <222> 1, 2, 3, 5, 6, 7, 8, 9, 10, 12, 13, 14, 15, 16, 19, 20, 21,  
 22, 24, 25, 26, 27, 28, 29, 30, 31, 33  
 <223> Xaa = Any Amino Acid

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 1 5 10 15  
 Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys  
 20 25 30  
 Xaa

<210> 61  
 <211> 439  
 <212> DNA  
 <213> Paecilomyces sp.

<400> 61  
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 aaatctccgc cgtcattgtc gcactcttcg ccagcgccgc catggccggc aagatctgca 120  
 ctctgtctgg agttgtacgt attttcatcc atttccctca ccactcctct aacatgaagc 180  
 aactttctct tctctctaga aatgtccgc ggctcttct tgtgccccg gacttcgctg 240  
 catcggcgcc gtcaacgtaa gtcaccatgg atctggcaag cgagaccata acatgacgca 300  
 gtatactaac cctggccggt atagaacaag gttgtgagtc gacatgttkt acaacctcta 360  
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 gtgggataag tatgcttcg 439

<210> 62  
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 <212> DNA  
 <213> Paecilomyces sp.

<400> 62  
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 cgccgtcatt gtcgcactct tcgccagcgc cgccatggcc ggcaagatct gcactcctgc 180  
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 caacaacaag gtttgccggt aattctagtg tcgcaacttt tgagcgtggg ataagtatgc 300  
 ttcgttcggt gtatggagtt ctctccgga gtttaagctc ggccgggtcga cagcgggtct 360  
 gctatacttg atcttacagc gatactattg atagaaatgc acatcttcat tcatgcgtca 420  
 tgaaaaaaaa aaaaaaaaa 438

<210> 63  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> INSECTICIDAL PROTEIN MOTIF

<400> 63

Leu Pro Cys Cys Pro Gly  
1 5

<210> 64

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> INSECTICIDAL PROTEIN MOTIF

<400> 64

Ile Cys Thr Pro Ala  
1 5

<210> 65

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN REGION N-TERMINAL

<221> VARIANT

<222> 1, 2

<223> Xaa = Any Amino Acid

<400> 65

Xaa Xaa Ile Cys Thr  
1 5